

SEQUENCE LISTING

<110> CO, MAN SUNG

VASQUEZ, MAXIMILIANO

<120> ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND FACTOR
MONOCLONAL ANTIBODY

<130> 202617US0PCT

<140> 09/763,129

<141> 2001-02-20

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<150> 09/136,315

<151> 1998-08-19

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 417

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(417)

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1 5 10 15	
cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act	96
Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr	
20 25 30	
gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt	144
Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser	
35 40 45	
aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa	192
Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
50 55 60	
tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca	240
Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro	
65 70 75 80	
tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg	288
Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr	
85 90 95	
ctg tac ctg caa atg agt caa gtg aga tct gag gac aca gcc ctt tac	336
Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr	
100 105 110	
tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac	384
Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr	
115 120 125	
tgg ggc caa ggg act ctg gtc tct gtc tcg cca	417
Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro	
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<210> 2

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Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
35 40 45

Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

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Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
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Asp	Ala	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	
			20					25					30			
gta	tct	gtg	gga	gaa	act	gtc	acc	atc	aca	tgt	cga	gca	agt	gag	aat	144
Val	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Asn	
		35					40					45				
att	tac	aat	aat	tta	gct	tgg	tat	cag	cag	aga	cag	gga	aaa	tct	cct	192
Ile	Tyr	Asn	Asn	Leu	Ala	Trp	Tyr	Gln	Gln	Arg	Gln	Gly	Lys	Ser	Pro	
	50					55					60					
cag	ctc	ctg	gtc	tat	gct	gca	aca	aac	tta	gca	gat	ggt	gtg	cca	tca	240
Gln	Leu	Leu	Val	Tyr	Ala	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	Pro	Ser	
65					70					75					80	
agg	ttc	agt	ggc	agt	gga	tca	ggc	aca	cag	tat	tcc	ctc	aag	atc	gac	288
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Tyr	Ser	Leu	Lys	Ile	Asp	
				85					90					95		
agc	ctg	cag	tct	gaa	gat	ttt	ggg	agt	tat	tac	tgt	caa	cat	ttg	tgg	336
Ser	Leu	Gln	Ser	Glu	Asp	Phe	Gly	Ser	Tyr	Tyr	Cys	Gln	His	Leu	Trp	
			100					105					110			
act	tct	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa		381
Thr	Ser	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
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<213> Mus musculus

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Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
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Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
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Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
 35 40 45

Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
 50 55 60

Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
 85 90 95

Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
 100 105 110

Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

<210> 5

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<212> DNA

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<222> (1)..(417)

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atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc	48
Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val	
1 5 10 15	
cag tgt gag gtg caa ctt gtc gag tct gga ggt gga cta gtg cag cct	96
Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro	
20 25 30	
gga gga tca ctg aga ctc tcc tgt gca gcc tca gga ttc gat ttt agt	144
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser	
35 40 45	
aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag	192
Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
50 55 60	
tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca	240
Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro	
65 70 75 80	
tct cta aag gat aaa ttc acc atc tcc aga gac aac gcc aaa aat acg	288
Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr	
85 90 95	
ctg tac ctg caa atg aac tca ttg aga gct gag gac acg gcc gtt tac	336
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr	
100 105 110	
tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac	384
Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr	
115 120 125	
tgg ggc caa ggg act ctg gtc acc gtc tcc tca	417
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Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
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Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
35 40 45

Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<222> (1)..(381)

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1 5 10 15	
gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct	96
Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser	
20 25 30	
gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat	144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn	
35 40 45	
att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct	192
Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro	
50 55 60	
aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca	240
Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser	
65 70 75 80	
agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser	
85 90 95	
agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg	336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp	
100 105 110	
act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa	381
Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys	
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<210> 8

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Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Trp Leu Thr
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Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
35 40 45

Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
100 105 110

Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125